

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Koji YANAI et al.
- (ii) TITLE OF INVENTION: β -FRUCTOFURANOSIDASE AND ITS GENE,
METHOD OF ISOLATING β -FRUCTOFURANOSIDASE GENE, SYSTEM
FOR PRODUCING β -FRUCTOFURANOSIDASE, AND
 β -FRUCTOFURANOSIDASE VARIANT
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 - (B) STREET: 2033 K Street, N.W., Suite 800
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: NEW
 - (B) FILING DATE: November 23, 2001
- (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/142,623

(B) FILING DATE: September 10, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lee Cheng

(B) REGISTRATION NUMBER: 40,949

(C) REFERENCE/DOCKET NUMBER: 2001-1611

(ix) TELECOMMUNICATION INFORMATION:

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(B) TELEFAX: 202-721-8250

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acid residues

(B) TYPE: amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1

(ATCC 20611)

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..635

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Tyr His Leu Asp Thr Thr Ala Pro Pro Pro Thr Asn Leu Ser Thr
1 5 10 15
Leu Pro Asn Asn Thr Leu Phe His Val Trp Arg Pro Arg Ala His Ile
20 25 30
Leu Pro Ala Glu Gly Gln Ile Gly Asp Pro Cys Ala His Tyr Thr Asp
35 40 45
Pro Ser Thr Gly Leu Phe His Val Gly Phe Leu His Asp Gly Asp Gly
50 55 60
Ile Ala Gly Ala Thr Thr Ala Asn Leu Ala Thr Tyr Thr Asp Thr Ser
65 70 75 80
Asp Asn Gly Ser Phe Leu Ile Gln Pro Gly Gly Lys Asn Asp Pro Val
85 90 95
Ala Val Phe Asp Gly Ala Val Ile Pro Val Gly Val Asn Asn Thr Pro
100 105 110
Thr Leu Leu Tyr Thr Ser Val Ser Phe Leu Pro Ile His Trp Ser Ile
115 120 125
Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ala Arg Asp
130 135 140
Gly Gly Arg Arg Phe Asp Lys Leu Asp Gln Gly Pro Val Ile Ala Asp
145 150 155 160
His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro Phe Val Phe
165 170 175
Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu Glu Val Ala
180 185 190

Arg	Asn	Glu	Thr	Ala	Val	Gln	Gln	Ala	Val	Asp	Gly	Trp	Thr	Glu	Lys
195					200					205					
Asn	Ala	Pro	Trp	Tyr	Val	Ala	Val	Ser	Gly	Gly	Val	His	Gly	Val	Gly
210					215					220					
Pro	Ala	Gln	Phe	Leu	Tyr	Arg	Gln	Asn	Gly	Gly	Asn	Ala	Ser	Glu	Phe
225					230					235					240
Gln	Tyr	Trp	Glu	Tyr	Leu	Gly	Glu	Trp	Trp	Gln	Glu	Ala	Thr	Asn	Ser
245					250					255					
Ser	Trp	Gly	Asp	Glu	Gly	Thr	Trp	Ala	Gly	Arg	Trp	Gly	Phe	Asn	Phe
260					265					270					
Glu	Thr	Gly	Asn	Val	Leu	Phe	Leu	Thr	Glu	Glu	Gly	His	Asp	Pro	Gln
275					280					285					
Thr	Gly	Glu	Val	Phe	Val	Thr	Leu	Gly	Thr	Glu	Gly	Ser	Gly	Leu	Pro
290					295					300					
Ile	Val	Pro	Gln	Val	Ser	Ser	Ile	His	Asp	Met	Leu	Trp	Ala	Ala	Gly
305					310					315					320
Glu	Val	Gly	Val	Gly	Ser	Glu	Gln	Glu	Gly	Ala	Lys	Val	Glu	Phe	Ser
325					330					335					
Pro	Ser	Met	Ala	Gly	Phe	Leu	Asp	Trp	Gly	Phe	Ser	Ala	Tyr	Ala	Ala
340					345					350					
Ala	Gly	Lys	Val	Leu	Pro	Ala	Ser	Ser	Ala	Val	Ser	Lys	Thr	Ser	Gly
355					360					365					
Val	Glu	Val	Asp	Arg	Tyr	Val	Ser	Phe	Val	Trp	Leu	Thr	Gly	Asp	Gln
370					375					380					

Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly Trp Thr Gly
 385 390 395 400
 Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val Glu Asn Val
 405 410 415
 Val Asp Asn Glu Leu Val Arg Glu Glu Gly Val Ser Trp Val Val Gly
 420 425 430
 Glu Ser Asp Asn Gln Thr Ala Arg Leu Arg Thr Leu Gly Ile Thr Ile
 435 440 445
 Ala Arg Glu Thr Lys Ala Ala Leu Leu Ala Asn Gly Ser Val Thr Ala
 450 455 460
 Glu Glu Asp Arg Thr Leu Gln Thr Ala Ala Val Val Pro Phe Ala Gln
 465 470 475 480
 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Gln Leu Glu Phe Pro
 485 490 495
 Ala Ser Ala Arg Ser Ser Pro Leu Gln Ser Gly Phe Glu Ile Leu Ala
 500 505 510
 Ser Glu Leu Glu Arg Thr Ala Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
 515 520 525
 Leu Val Val Asp Arg Ser Gln Thr Ser Ala Ala Ala Pro Thr Asn Pro
 530 535 540
 Gly Leu Asp Ser Phe Thr Glu Ser Gly Lys Leu Arg Leu Phe Asp Val
 545 550 555 560
 Ile Glu Asn Gly Gln Glu Gln Val Glu Thr Leu Asp Leu Thr Val Val
 565 570 575

Val Asp Asn Ala Val Val Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu		
580	585	590
Ser Thr Trp Ala Arg Ser Trp Tyr Asp Asn Ser Thr Gln Ile Arg Phe		
595	600	605
Phe His Asn Gly Glu Gly Glu Val Gln Phe Arg Asn Val Ser Val Ser		
610	615	620
Glu Gly Leu Tyr Asn Ala Trp Pro Glu Arg Asn		
625	630	635

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 1905
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCGTCCCCGC TCCAGTCCGG GTTCGAAATC CTGGCGTCGG AGCTGGAGCG CACGGCCATC 1560
TACTACCAGT TCAGCAACGA GTCGCTGGTC GTCGACCGCA GCCAGACTAG TGCGGCGGCG 1620
CCCACGAACC CCGGGCTGGA TAGCTTTACT GAGTCCGGCA AGTTGCGGTT GTTCGACGTG 1680
ATCGAGAACG GCCAGGAGCA GGTTCGAGACG TTGGATCTCA CTGTCGTCGT GGATAACGCG 1740
GTTGTCGAGG TGTATGCCAA CGGGCGCTTT GCGTTGAGCA CCTGGGCGAG ATCGTGGTAC 1800
GACAACTCCA CCCAGATCCG CTTCTTCCAC AACGGCGAGG GCGAGGTGCA GTTCAGGAAT 1860
GTCTCCGTGT CGGAGGGGCT CTATAACGCC TGGCCGGAGA GAAAT 1905

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Asp Gln Gly Pro Val Ile Ala Asp His Pro Phe Ala Val Asp Val
1 5 10 15
Thr Ala Phe Arg
20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1

(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser
1 5 10 15
Ala Tyr Ala Ala
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Gln Thr Val Glu Asn Val Val Asp Asn Glu Leu Val Arg Glu Glu
1 5 10 15
Gly Val Ser Trp
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acid residues
(B) TYPE: Amino acid
(C) STRANDEDNESS: Not relevant
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Leu Leu Ala Xaa Gly Ser Val Thr Ala Glu Glu Asp Arg Thr
1 5 10 15
Leu Gln Thr Ala
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Tyr His Leu Asp Thr

1

5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCGCSGAYC AYCCSTTYGC 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCRTTRTCSA CSACRTTYTC 20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(ix) FEATURE:

- (A) NAME/KEY: P CDS(partial amino acid sequence)
- (B) LOCATION: 1 .. 788
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATC GCC GAC CAC CCC TTC GCC GTC GAC GTC ACC GCC TTC CGC GAT CCG	48
Ile Ala Asp His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro	
1 5 10 15	
TTT GTC TTC CGC AGT GCC AAG TTG GAT GTG CTG CTG TCG TTG GAT GAG	96
Phe Val Phe Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu	
20 25 30	
GAG GTG GCG CGG AAT GAG ACG GCC GTG CAG CAG GCC GTC GAT GGC TGG	144
Glu Val Ala Arg Asn Glu Thr Ala Val Gln Gln Ala Val Asp Gly Trp	
35 40 45	
ACC GAG AAG AAC GCC CCC TGG TAT GTC GCG GTC TCT GGC GGG GTG CAC	192
Thr Glu Lys Asn Ala Pro Trp Tyr Val Ala Val Ser Gly Gly Val His	
50 55 60	
GGC GTC GGG CCC GCG CAG TTC CTC TAC CGC CAG AAC GGC GGG AAC GCT	240
Gly Val Gly Pro Ala Gln Phe Leu Tyr Arg Gln Asn Gly Gly Asn Ala	
65 70 75 80	
TCC GAG TTC CAG TAC TGG GAG TAC CTC GGG GAG TGG TGG CAG GAG GCG	288
Ser Glu Phe Gln Tyr Trp Glu Tyr Leu Gly Glu Trp Trp Gln Glu Ala	
85 90 95	
ACC AAC TCC AGC TGG GGC GAC GAG GGC ACC TGG GCC GGG CGC TGG GGG	336
Thr Asn Ser Ser Trp Gly Asp Glu Gly Thr Trp Ala Gly Arg Trp Gly	
100 105 110	
TTC AAC TTC GAG ACG GGG AAT GTG CTC TTC CTC ACC GAG GAG GGC CAT	384
Phe Asn Phe Glu Thr Gly Asn Val Leu Phe Leu Thr Glu Glu Gly His	
115 120 125	

GAC CCC CAG ACG GGC GAG GTG TTC GTC ACC CTC GGC ACG GAG GGG TCT	432
Asp Pro Gln Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser	
130 135 140	
GGC CTG CCA ATC GTG CCG CAG GTC TCC AGT ATC CAC GAT ATG CTG TGG	480
Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp	
145 150 155 160	
GCG GCG GGT GAG GTC GGG GTG GGC AGT GAG CAG GAG GGT GCC AAG GTC	528
Ala Ala Gly Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val	
165 170 175	
GAG TTC TCC CCC TCC ATG GCC GGG TTT CTG GAC TGG GGG TTC AGC GCC	576
Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala	
180 185 190	
TAC GCT GCG GCG GGC AAG GTG CTG CCG GCC AGC TCG GCG GTG TCG AAG	624
Tyr Ala Ala Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys	
195 200 205	
ACC AGC GGC GTG GAG GTG GAT CGG TAT GTC TCG TTC GTC TGG TTG ACG	672
Thr Ser Gly Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr	
210 215 220	
GGC GAC CAG TAC GAG CAG GCG GAC GGG TTC CCC ACG GCC CAG CAG GGG	720
Gly Asp Gln Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly	
225 230 235 240	
TGG ACG GGG TCG CTG CTG CTG CCG CGC GAG CTG AAG GTG CAG ACG GTG	768
Trp Thr Gly Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val	
245 250 255	

GAG AAC GTC GTC GAC AAC GA

Glu Asn Val Val Asp Asn

260

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Penicillium roqueforti* IAM7254

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 565

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val	Asp	Phe	His	Thr	Pro	Ile	Asp	Tyr	Asn	Ser	Ala	Pro	Pro	Asn	Leu
1				5					10					15	
Ser	Thr	Leu	Ala	Asn	Ala	Ser	Leu	Phe	Lys	Thr	Trp	Arg	Pro	Arg	Ala
			20					25					30		
His	Leu	Leu	Pro	Pro	Ser	Gly	Asn	Ile	Gly	Asp	Pro	Cys	Gly	His	Tyr
			35					40					45		

Thr Asp Pro Lys Thr Gly Leu Phe His Val Gly Trp Leu Tyr Ser Gly
 50 55 60
 Ile Ser Gly Ala Thr Thr Asp Asp Leu Val Thr Tyr Lys Asp Leu Asn
 65 70 75 80
 Pro Asp Gly Ala Pro Ser Ile Val Ala Gly Gly Lys Asn Asp Pro Leu
 85 90 95
 Ser Val Phe Asp Gly Ser Val Ile Pro Ser Gly Ile Asp Gly Met Pro
 100 105 110
 Thr Leu Leu Tyr Thr Ser Val Ser Tyr Leu Pro Ile His Trp Ser Ile
 115 120 125
 Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ser Tyr Asp
 130 135 140
 Gly Gly His Asn Phe Thr Lys Leu Asn Gln Gly Pro Val Ile Pro Thr
 145 150 155 160
 Pro Pro Phe Ala Leu Asn Val Thr Ala Phe Arg Asp Pro Tyr Val Phe
 165 170 175
 Gln Ser Pro Ile Leu Asp Lys Ser Val Asn Ser Thr Gln Gly Thr Trp
 180 185 190
 Tyr Val Ala Ile Ser Gly Gly Val His Gly Val Gly Pro Cys Gln Phe
 195 200 205
 Leu Tyr Arg Gln Asn Asp Ala Asp Phe Gln Tyr Trp Glu Tyr Leu Gly
 210 215 220
 Gln Trp Trp Lys Glu Pro Leu Asn Thr Thr Trp Gly Lys Gly Asp Trp
 225 230 235 240

Ala Gly Gly Trp Gly Phe Asn Phe Glu Val Gly Asn Val Phe Ser Leu

245

250

255

Asn Ala Glu Gly Tyr Ser Glu Asp Gly Glu Ile Phe Ile Thr Leu Gly

260

265

270

Ala Glu Gly Ser Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile Arg

275

280

285

Asp Met Leu Trp Val Thr Gly Asn Val Thr Asn Asp Gly Ser Val Thr

290

295

300

Phe Lys Pro Thr Met Ala Gly Val Leu Asp Trp Gly Val Ser Ala Tyr

305

310

315

320

Ala Ala Ala Gly Lys Ile Leu Pro Ala Ser Ser Gln Ala Ser Thr Lys

325

330

335

Ser Gly Ala Pro Asp Arg Phe Ile Ser Tyr Val Trp Leu Thr Gly Asp

340

345

350

Leu Phe Glu Gln Val Lys Gly Phe Pro Thr Ala Gln Gln Asn Trp Thr

355

360

365

Gly Ala Leu Leu Leu Pro Arg Glu Leu Asn Val Arg Thr Ile Ser Asn

370

375

380

Val Val Asp Asn Glu Leu Ser Arg Glu Ser Leu Thr Ser Trp Arg Val

385

390

395

400

Ala Arg Glu Asp Ser Gly Gln Ile Asp Leu Glu Thr Met Gly Ile Ser

405

410

415

Ile Ser Arg Glu Thr Tyr Ser Ala Leu Thr Ser Gly Ser Ser Phe Val

420

425

430

Glu Ser Gly Lys Thr Leu Ser Asn Ala Gly Ala Val Pro Phe Asn Thr
 435 440 445
 Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Asn Ile Ser Phe Pro
 450 455 460
 Thr Ser Ala Arg Asp Ser Gly Ile Gln Ala Gly Phe Gln Val Leu Ser
 465 470 475 480
 Ser Ser Leu Glu Ser Thr Thr Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
 485 490 495
 Ile Ile Val Asp Arg Ser Asn Thr Ser Ala Ala Ala Arg Thr Thr Ala
 500 505 510
 Gly Ile Leu Ser Asp Asn Glu Ala Gly Arg Leu Arg Leu Phe Asp Val
 515 520 525
 Leu Arg Asn Gly Lys Glu Gln Val Glu Thr Leu Glu Leu Thr Ile Val
 530 535 540
 Val Asp Asn Ser Val Leu Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu
 545 550 555 560
 Gly Thr Trp Ala Arg
 565

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1695 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Penicillium roqueforti* IAM7254

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 1695

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGATTTCC ATACCCCGAT TGA CTATAAC TCGGCTCCGC CAAACCTTTC TACCCTGGCA 60
AACGCATCTC TTTTCAAGAC ATGGAGACCC AGAGCCCATC TTCTCCCTCC ATCTGGGAAC 120
ATAGGCGACC CGTGCGGGCA CTATACCGAT CCCAAGACTG GTCTCTTCCA CGTGGGTTGG 180
CTTTACAGTG GGATTTCTGGG AGCGACAACC GACGATCTCG TTACCTATAA AGACCTCAAT 240
CCCGATGGAG CCCCCTCAAT TGTTCAGGA GGAAAGAACG ACCCTCTTTC TGTCTTCGAT 300
GGCTCGGTCA TTCCAAGCGG TATAGACGGC ATGCCAACTC TTCTGTATAC CTCTGTATCA 360
TACCTCCCAA TCCACTGGTC CATCCCCTAC ACCCGGGGAA GCGAGACACA ATCCTTGGCC 420
GTTTCCTATG ACGGTGGTCA CAACTTCACC AAGCTCAACC AAGGGCCCGT GATCCCTACG 480
CCTCCGTTTG CTCTCAATGT CACCGCTTTC CGTGACCCCT ACGTTTTCCTA AAGCCCAATT 540
CTGGACAAAT CTGTCAATAG TACCCAAGGA ACATGGGTATG TCGCCATATC TGGCGGTGTC 600
CACGGTGTCTG GACCTTGTCG GTTCCTCTAC CGTCAGAACG ACGCAGATTT TCAATATTGG 660
GAATATCTCG GGCAATGGTG GAAGGAGCCC CTTAATACCA CTTGGGGAAA GGGTGACTGG 720
GCCGGGGGTT GGGGCTTCAA CTTTGAGGTT GGCAACGTCT TTAGTCTGAA TGCAGAGGGG 780
TATAGTGAAG ACGGCGAGAT ATTCATAACC CTCGGTGCTG AGGGTTCGGG ACTTCCCATC 840
GTTCTCAAG TCTCCTCTAT TCGCGATATG CTGTGGGTGA CCGGCAATGT CACAAATGAC 900
GGCTCTGTCA CTTTCAAGCC AACCATGGCG GGTGTGCTTG ACTGGGGCGT GTCGGCATAT 960
GCTGCTGCAG GCAAGATCTT GCCGGCCAGC TCTCAGGCAT CCACAAAGAG CGGTGCCCCC 1020

GATCGGTTCA	TTTCCTATGT	CTGGCTCACT	GGAGATCTAT	TCGAGCAAGT	GAAAGGATTC	1080
CCTACCGCTC	AACAAAAC TG	GACCGGGGCC	CTCTTACTGC	CGCGAGAGCT	GAATGTCCGC	1140
ACTATCTCTA	ACGTGGTGGA	TAACGAACTT	TCGCGTGAGT	CCTTGACATC	GTGGCGCGTG	1200
GCCCCGGAAG	ACTCTGGTCA	GATCGACCTT	GAAACAATGG	GAATCTCAAT	TTCCAGGGAG	1260
ACTTACAGCG	CTCTCACATC	CGGCTCATCT	TTTGTGAGT	CTGGTAAAAC	GTTGTCGAAT	1320
GCTGGAGCAG	TGCCCTTCAA	TACCTACCCC	TCAAGCAAGT	TCTTCGTGCT	GACAGCAAAT	1380
ATATCTTTCC	CGACCTCTGC	CCGTGACTCT	GGCATCCAGG	CTGGTTTCCA	GGTTTTATCC	1440
TCTAGTCTTG	AGTCTACAAC	TATCTACTAC	CAATTCTCCA	ACGAGTCCAT	CATCGTCGAC	1500
CGCAGCAACA	CGAGTGCTGC	GGCGAGAACA	ACTGCTGGGA	TCCTCAGTGA	TAACGAGGCG	1560
GGACGTCTGC	GCCTCTTCGA	CGTGTTGCGA	AATGGAAAAG	AACAGGTTGA	AACTTTGGAG	1620
CTCACTATCG	TGGTGGATAA	TAGTGACTG	GAAGTATATG	CCAATGGACG	CTTTGCTCTA	1680
GGCACTTGGG	CTCGG					1695

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Scopulariopsis brevicaulis* IF04843

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 574

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Pro Thr Ser Leu Ser Ile Asp Asn Ser Thr Tyr Pro Ser Ile Asp
1 5 10 15
Tyr Asn Ser Ala Pro Pro Asn Leu Ser Thr Leu Ala Asn Asn Ser Leu
20 25 30
Phe Glu Thr Trp Arg Pro Arg Ala His Val Leu Pro Pro Gln Asn Gln
35 40 45
Ile Gly Asp Pro Cys Met His Tyr Thr Asp Pro Glu Thr Gly Ile Phe
50 55 60
His Val Gly Trp Leu Tyr Asn Gly Asn Gly Ala Ser Gly Ala Thr Thr
65 70 75 80
Glu Asp Leu Val Thr Tyr Gln Asp Leu Asn Pro Asp Gly Ala Gln Met
85 90 95
Ile Leu Pro Gly Gly Val Asn Asp Pro Ile Ala Val Phe Asp Gly Ala
100 105 110
Val Ile Pro Ser Gly Ile Asp Gly Lys Pro Thr Met Met Tyr Thr Ser
115 120 125
Val Ser Tyr Met Pro Ile Ser Trp Ser Ile Ala Tyr Thr Arg Gly Ser
130 135 140
Glu Thr His Ser Leu Ala Val Ser Ser Asp Gly Gly Lys Asn Phe Thr
145 150 155 160
Lys Leu Val Gln Gly Pro Val Ile Pro Ser Pro Pro Phe Gly Ala Asn
165 170 175

Val Thr Ser Trp Arg Asp Pro Phe Leu Phe Gln Asn Pro Gln Phe Asp
 180 185 190
 Ser Leu Leu Glu Ser Glu Asn Gly Thr Trp Tyr Thr Val Ile Ser Gly
 195 200 205
 Gly Ile His Gly Asp Gly Pro Ser Ala Phe Leu Tyr Arg Gln His Asp
 210 215 220
 Pro Asp Phe Gln Tyr Trp Glu Tyr Leu Gly Pro Trp Trp Asn Glu Glu
 225 230 235 240
 Gly Asn Ser Thr Trp Gly Ser Gly Asp Trp Ala Gly Arg Trp Gly Tyr
 245 250 255
 Asn Phe Glu Val Ile Asn Ile Val Gly Leu Asp Asp Asp Gly Tyr Asn
 260 265 270
 Pro Asp Gly Glu Ile Phe Ala Thr Val Gly Thr Glu Trp Ser Phe Asp
 275 280 285
 Pro Ile Lys Pro Gln Ala Ser Asp Asn Arg Glu Met Leu Trp Ala Ala
 290 295 300
 Gly Asn Met Thr Leu Glu Asp Gly Asp Ile Lys Phe Thr Pro Ser Met
 305 310 315 320
 Ala Gly Tyr Leu Asp Trp Gly Leu Ser Ala Tyr Ala Ala Ala Gly Lys
 325 330 335
 Glu Leu Pro Ala Ser Ser Lys Pro Ser Gln Lys Ser Gly Ala Pro Asp
 340 345 350
 Arg Phe Val Ser Tyr Leu Trp Leu Thr Gly Asp Tyr Phe Glu Gly His
 355 360 365

Asp Phe Pro Thr Pro Gln Gln Asn Trp Thr Gly Ser Leu Leu Leu Pro
 370 375 380
 Arg Glu Leu Ser Val Gly Thr Ile Pro Asn Val Val Asp Asn Glu Leu
 385 390 395 400
 Ala Arg Glu Thr Gly Ser Trp Arg Val Gly Thr Asn Asp Thr Gly Val
 405 410 415
 Leu Glu Leu Val Thr Leu Lys Gln Glu Ile Ala Arg Glu Thr Leu Ala
 420 425 430
 Glu Met Thr Ser Gly Asn Ser Phe Thr Glu Ala Ser Arg Asn Val Ser
 435 440 445
 Ser Pro Gly Ser Thr Ala Phe Gln Gln Ser Leu Asp Ser Lys Phe Phe
 450 455 460
 Val Leu Thr Ala Ser Leu Ser Phe Pro Ser Ser Ala Arg Asp Ser Asp
 465 470 475 480
 Leu Lys Ala Gly Phe Glu Ile Leu Ser Ser Glu Phe Glu Ser Thr Thr
 485 490 495
 Val Tyr Tyr Gln Phe Ser Asn Glu Ser Ile Ile Ile Asp Arg Ser Asn
 500 505 510
 Ser Ser Ala Ala Ala Leu Thr Thr Asp Gly Ile Asp Thr Arg Asn Glu
 515 520 525
 Phe Gly Lys Met Arg Leu Phe Asp Val Val Glu Gly Asp Gln Glu Arg
 530 535 540
 Ile Glu Thr Leu Asp Leu Thr Ile Val Val Asp Asn Ser Ile Val Glu
 545 550 555 560

Val His Ala Asn Gly Arg Phe Ala Leu Ser Thr Trp Val Arg

565

570

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1722 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double stranded

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Scopulariopsis brevicaulis* IFO4843

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 1722

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAACCTACGT CTCTGTCAAT CGACAATTCC ACGTATCCTT CTATCGACTA CAACTCCGCC	60
CCTCCAAACC TCTCGACTCT TGCCAACAAC AGCCTCTTCG AGACATGGAG GCCGAGGGCA	120
CACGTCCTTC CGCCCCAGAA CCAGATCGGC GATCCGTGTA TGCACTACAC CGACCCCGAG	180
ACAGGAATCT TCCACGTCGG CTGGCTGTAC AACGGCAATG GCGCTTCCGG CGCCACGACC	240
GAGGATCTCG TCACCTATCA GGATCTCAAC CCCGACGGAG CGCAGATGAT CCTTCCGGGT	300
GGTGTGAATG ACCCCATTGC TGTCTTTGAC GGCGCGGTTA TTCCCAGTGG CATTGATGGG	360
AAACCCACCA TGATGTATAC CTCGGTGTCA TACATGCCCA TCTCCTGGAG CATCGCTTAC	420
ACCAGGGGAA GCGAGACCCA CTCTCTCGCA GTGTCTGTCG ACGGCGGTAA GAACTTCACC	480

AAGCTGGTGC	AGGGCCCCGT	CATTCCTTCG	CCTCCCTTCG	GCGCCAACGT	GACCAGCTGG	540
CGTGACCCCT	TCCTGTTCCA	AAACCCCCAG	TTGACTCTC	TCCTCGAAAG	CGAGAACGGC	600
ACGTGGTACA	CCGTTATCTC	TGGTGGCATC	CACGGTGACG	GCCCCCTCCG	GTTCCCTCTAC	660
CGTCAGCACG	ACCCCGACTT	CCAGTACTGG	GAGTACCTTG	GACCGTGGTG	GAACGAGGAA	720
GGGAACTCGA	CCTGGGGCAG	CGGTGACTGG	GCTGGCCGGT	GGGGCTACAA	CTTCGAGGTC	780
ATCAACATTG	TCGGTCTTGA	CGATGATGGC	TACAACCCCG	ACGGTGAAAT	CTTTGCCACG	840
GTAGGTACCG	AATGGTCGTT	TGACCCCATC	AAACCGCAGG	CCTCGGACAA	CAGGGAGATG	900
CTCTGGGCCG	CGGGCAACAT	GACTCTCGAG	GACGGCGATA	TCAAGTTCAC	GCCAAGCATG	960
GCGGGCTACC	TCGACTGGGG	TCTATCGGCG	TATGCCGCCG	CTGGCAAGGA	GCTGCCCCGCT	1020
TCTTCAAAGC	CTTCGCAGAA	GAGCGGTGCG	CCGGACCGGT	TCGTGTCGTA	CCTGTGGGCTC	1080
ACCGGTGACT	ACTTCGAGGG	CCACGACTTC	CCCACCCCGC	AGCAGAATTG	GACCGGCTCG	1140
CTTTTGCTTC	CGCGTGAGCT	GAGCGTCGGG	ACGATTCCCA	ACGTTGTCGA	CAACGAGCTT	1200
GCTCGCGAGA	CGGGCTCTTG	GAGGGTTGGC	ACCAACGACA	CTGGCGTGCT	TGAGCTGGTC	1260
ACTCTGAAGC	AGGAGATTGC	TCGCGAGACG	CTGGCTGAAA	TGACCAGCGG	CAACTCCTTC	1320
ACCGAGGCGA	GCAGGAATGT	CAGCTCGCCC	GGATCTACCG	CCTTCCAGCA	GTCCCTGGAT	1380
TCCAAGTTCT	TCGTCTTGAC	CGCCTCGCTC	TCCTTCCCTT	CGTCGGCTCG	CRACTCCGAC	1440
CTCAAGGCTG	GTTTCGAGAT	CCTGTCTGCC	GAGTTTGAGT	CGACCACGGT	CTACTACCAG	1500
TTTTCCAACG	AGTCCATCAT	CATTGACCGG	AGCAACTCGA	GTGCTGCCGC	CTTGACTACC	1560
GATGGAATCG	ACACCCGCAA	CGAGTTTGGC	AAGATGCGCC	TGTTTGATGT	TGTCGAGGGT	1620
GACCAGGAGC	GTATCGAGAC	GCTCGATCTC	ACTATTGTGG	TTGATAACTC	GATCGTTGAG	1680
GTTCATGCCA	ACGGGCGATT	CGCTCTGAGC	ACTTGGGTTC	GG		1722

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGAATTCCA ATGAAGCTCA CCACTACC

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGATCCCG GTCAATTTCT CTCC

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTGACCGG TGTTTCATCC

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCGGTTGTC ATAGATGTGG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAATCCAGGA GGATCCCAAT GAAG

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

81

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGACCGGGAT CCGGGCATGC AG

22

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGTCGTCT AGAGGTTGTC ACTT

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCTATTGGG GTCCATGGCC C

21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAACTGCTGG CATCCTCAGT GA

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGATCCAT GAAGCTATCA AATGCAATCA

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

83

- (A) LENGTH: 26 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCGGATCCTT ACCGAGCCCA AGTGCC

26

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGGATCCAA TGAAGCTCAC CACTACC

27

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGATCCCG GTCAATTTCT CTCC

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCACCGCCT GGCGCGATCC G

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCACGGAGT GGTCTGGCC

19

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTCCAGTATC AAGGATATGC TGTG

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGACCAGTAC AAGCAGGCGG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCCAGTATCC GCGATATGCT G

21

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGCACGGAG GTTTCTGGCC TGC

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGCACGGAG GAGTCTGGCC TGC

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGGCACGGAG GATTCTGGCC TGC

23

CGGCACGGAG GATTCTGGCC TGC